

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (1) AUCKLAND UNISERVICES LIMITED, a duly incorporated New Zealand company c/- The University of Auckland, 58 Symonds Street, Auckland, New Zealand.
- (2) TITLE OF INVENTION: Developmental Tyrosine Kinases and their Ligands.
- (3) NUMBER OF SEQUENCES: 16
- (4) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: A J PARK & SON
 - (B) STREET: HUDDART PARKER BUILDING, POST OFFICE SQUARE
 - (C) CITY: P O BOX 949, WELLINGTON
 - (D) COUNTRY: NEW ZEALAND
- (5) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: 3.5,DS,HD FLOPPY DISC
 - (B) COMPUTER: IBM PC COMPATIBLE
 - (C) OPERATION SYSTEM: MS-DOS
 - (D) SOFTWARE: WORD PERFECT 5.1 FOR DOS
- (6) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE: 16-FEBRUARY 1994
 - (C) CLASSIFICATION
- (7) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: BENNETT, MICHAEL R.
- (8) TELECOMMUNICATION INFORMATION
 - (A) TELEPHONE: (64 4) 473 8278
 - (B) TELEFAX: (64 4) 472 3358

(2) INFORMATION FOR SEQUENCE ID NO. 1:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 874 AMINO ACIDS
 - (B) TYPE: AMINO ACID
 - (C) TOPOLOGY: LINEAR
- (2) MOLECULE TYPE: PROTEIN
- (3) SEQUENCE DESCRIPTION: SEQ ID NO. 1:

Met	Gly	Trp	Pro	Gly	Leu	Arg	Pro	Leu	Leu	Leu	Ala	Gly
1				5					10			
Leu	Ala	Ser	Leu	Leu	Leu	Pro	Gly	Ser	Ala	Ala	Ala	Gly
	15					20					25	

Leu	Lys	Leu	Met	Gly	Ala	Pro	Val	Lys	Met	Thr	Val	Ser
Gln	Gly	Gln	Pro	Val	Lys	Leu	Asn	Cys	Ser	Val	Glu	Gly
40					45					50		
Met	Glu	Asp	Pro	Asp	Ile	His	Trp	Met	Lys	Asp	Gly	Thr
		55					60					65
Val	Val	Gln	Asn	Ala	Ser	Gln	Val	Ser	Ile	Ser	Ile	Ser
				70					75			
Glu	His	Ser	Trp	Ile	Gly	Leu	Leu	Ser	Leu	Lys	Ser	Val
	80					85					90	
Glu	Arg	Ser	Asp	Ala	Gly	Leu	Tyr	Trp	Cys	Gln	Val	Lys
			95					100				
Asp	Gly	Glu	Glu	Thr	Lys	Ile	Ser	Gln	Ser	Val	Trp	Leu
105					110					115		
Thr	Val	Glu	Gly	Val	Pro	Phe	Phe	Thr	Val	Glu	Pro	Lys
		120					125					130
Asp	Leu	Ala	Val	Pro	Pro	Asn	Ala	Pro	Phe	Gln	Leu	Ser
				135					140			
Cys	Glu	Ala	Val	Gly	Pro	Pro	Glu	Pro	Val	Thr	Ile	Tyr
	145					150					155	
Trp	Trp	Arg	Gly	Leu	Thr	Lys	Val	Gly	Gly	Pro	Ala	Pro
			160					165				
Ser	Pro	Ser	Val	Leu	Asn	Val	Thr	Gly	Val	Thr	Gln	Arg
170					175					180		
Thr	Glu	Phe	Ser	Cys	Glu	Ala	Arg	Asn	Ile	Lys	Gly	Leu
		185					190					195
Ala	Thr	Ser	Arg	Pro	Ala	Ile	Val	Arg	Leu	Gln	Ala	Pro
				200					205			
Pro	Ala	Ala	Pro	Phe	Asn	Thr	Thr	Val	Thr	Thr	Ile	Ser
	210					215					220	
Ser	Tyr	Asn	Ala	Ser	Val	Ala	Trp	Val	Pro	Gly	Ala	Asp
			225					230				
Gly	Leu	Ala	Leu	Leu	His	Ser	Cys	Thr	Val	Gln	Val	Ala
235					240					245		
His	Ala	Pro	Gly	Glu	Trp	Glu	Ala	Leu	Ala	Val	Val	Val
		250					255					260
Pro	Val	Pro	Pro	Phe	Thr	Cys	Leu	Leu	Arg	Asn	Leu	Ala
				265					270			
Pro	Ala	Thr	Asn	Tyr	Ser	Leu	Arg	Val	Arg	Cys	Ala	Asn
	275					280					285	
Ala	Leu	Gly	Pro	Ser	Pro	Tyr	Gly	Asp	Trp	Val	Pro	Phe
			290					295				
Gln	Thr	Lys	Gly	Leu	Ala	Pro	Ala	Arg	Ala	Pro	Gln	Asn
300					305					310		
Phe	His	Ala	Ile	Arg	Thr	Asp	Ser	Gly	Leu	Ile	Leu	Glu
		315					320					325
Trp	Glu	Glu	Val	Ile	Pro	Glu	Asp	Pro	Gly	Glu	Gly	Pro
				330					335			
Leu	Gly	Pro	Tyr	Lys	Leu	Ser	Trp	Val	Gln	Glu	Asn	Gly
	340					345					350	
Thr	Gln	Asp	Glu	Leu	Met	Val	Glu	Gly	Thr	Arg	Ala	Asn
			355					360				
Leu	Thr	Asp	Trp	Asp	Pro	Gln	Lys	Asp	Leu	Ile	Leu	Arg
365					370					375		
Val	Cys	Ala	Ser	Asn	Ala	Ile	Gly	Asp	Gly	Pro	Trp	Ser
		380					385					390
Gln	Pro	Leu	Val	Val	Ser	Ser	His	Asp	His	Ala	Gly	Arg
				395					400			
Gln	Gly	Pro	Pro	His	Ser	Arg	Thr	Ser	Trp	Val	Pro	Val
	405					410					415	
Val	Leu	Gly	Val	Leu	Thr	Ala	Leu	Ile	Thr	Ala	Ala	Ala
			420					425				
Leu	Ala	Leu	Ile	Leu	Leu	Arg	Lys	Arg	Arg	Lys	Glu	Thr
430					435					440		
Arg	Phe	Gly	Gln	Ala	Phe	Asp	Ser	Val	Met	Ala	Arg	Gly
		445					450					455
Glu	Pro	Ala	Val	His	Phe	Arg	Ala	Ala	Arg	Ser	Phe	Asn
				460					465			

Arg	Glu	Arg	Pro	Glu	Arg	Ile	Glu	Ala	Thr	Leu	Asp	Ser
Leu	Gly	Ile	Ser	Asp	Glu	Leu	Lys	Glu	Lys	Leu	Glu	Asp
Val	Leu	Ile	Pro	Glu	Gln	Gln	Phe	Thr	Leu	Gly	Arg	Met
495	Gly	Lys	Gly	Glu	500	Gly	Ser	Val	Arg	505	Ala	Gln
Leu	Lys	510	Gln	Asp	Gly	Ser	Phe	Val	Lys	Val	Ala	Val
Leu	Lys	Gln	Glu	525	Asp	Ile	Ile	Ala	Ser	Ser	Asp	Ile
Lys	Met	Leu	Lys	Ala	Asp	540	Ala	Cys	Met	Lys	Glu	Phe
Glu	Glu	Phe	Leu	Arg	Glu	Ala	Ala	555	Val	Gly	Val	Ser
Asp	His	Pro	His	Val	Ala	Lys	Leu	Val	Gly	570	Ser	Leu
560	Ser	Arg	Ala	Lys	Gly	Arg	Leu	Pro	Ile	Pro	Met	Val
Arg	Ser	575	Phe	Met	Lys	His	Gly	Asp	Leu	His	Ala	Phe
Ile	Leu	Pro	Arg	590	Ile	Gly	Glu	Asn	Pro	Phe	Asn	Leu
Leu	Leu	Ala	Ser	Arg	Ile	605	Glu	Asn	Pro	Phe	Asn	Leu
Pro	Leu	Gln	Thr	Leu	Val	Arg	Phe	Met	Val	Asp	Ile	Ala
Cys	Gly	Met	Glu	Tyr	Leu	Ser	Ser	Arg	Asn	Phe	Ile	His
625	Arg	Leu	Ala	Ala	Arg	Asn	Cys	Met	Leu	Ala	Glu	Asp
Arg	Asp	640	Cys	Val	Ala	Asp	Phe	Gly	Leu	Ser	Arg	Lys
Met	Thr	Val	Gly	Asp	Tyr	Tyr	Arg	Gln	Gly	Cys	Ala	Ser
Ile	Tyr	Ser	Gly	Asp	Tyr	670	Arg	Gln	Gly	Cys	Ala	Ser
Lys	Leu	Pro	Val	Lys	Trp	Leu	Ala	Leu	Glu	Ser	Leu	Ala
Asp	Asn	Leu	Tyr	Thr	Val	His	Ser	Asp	Val	Trp	Ala	Phe
690	Gly	Val	Thr	Met	Trp	Glu	Ile	Met	Thr	Arg	Gly	Gln
Gly	Val	705	Met	Trp	Glu	Ile	Met	710	Thr	Arg	Gly	Gln
Pro	Tyr	Ala	Gly	Ile	Glu	Asn	Ala	Glu	Ile	Tyr	Asn	Tyr
Leu	Ile	Gly	Gly	Asn	Arg	Leu	Lys	Gln	Pro	Pro	Glu	Cys
Met	Glu	Glu	Val	Tyr	Asp	Leu	Met	Tyr	Gln	Cys	Trp	Ser
Ala	Asp	Pro	Lys	Gln	Arg	Pro	Ser	Phe	Thr	Cys	Leu	Arg
755	Met	Glu	Leu	Glu	Asn	Ile	Leu	Gly	His	Leu	Ser	Val
Met	Glu	770	Glu	Asn	Ile	Leu	Gly	775	His	Leu	Ser	Val
Ser	Thr	Ser	Gln	Asp	Pro	Leu	Tyr	Ile	Asn	Ile	Glu	Arg
Ala	Glu	Gln	Pro	Thr	Glu	Ser	Gly	Ser	Pro	Glu	Leu	His
Gly	Gly	Glu	Arg	Ser	Ser	Ser	Glu	Ala	Gly	Asp	Gly	Ser
820	Val	Gly	Ala	Val	Gly	Gly	Ile	Pro	Ser	Asp	Ser	Arg
Tyr	Ile	Phe	Ser	Pro	Gly	Gly	Leu	Ser	Glu	Ser	Pro	Gly
Gln	Leu	Glu	Gln	Gln	Pro	Glu	Ser	Pro	Leu	Asn	Glu	Asn
Gln	Arg	Leu	Leu	Leu	Leu	Gln	Gln	Gly	Leu	Leu	Pro	His
Ser	Ser	Cys				865					870	

(3) INFORMATION FOR SEQUENCE ID NO. 2:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 850 AMINO ACIDS

(B) TYPE: AMINO ACID

(C) TOPOLOGY: LINEAR

(2) MOLECULE TYPE: PROTEIN

(3) SEQUENCE DESCRIPTION: SEQ ID NO. 2:

											Ala	Gly
											1	
Leu	Lys	Leu	Met	Gly	Ala	Pro	Val	Lys	Met	Thr	Val	Ser
		5					10					15
Gln	Gly	Gln	Pro	Val	Lys	Leu	Asn	Cys	Ser	Val	Glu	Gly
				20					25			
Met	Glu	Asp	Pro	Asp	Ile	His	Trp	Met	Lys	Asp	Gly	Thr
	30					35					40	
Val	Val	Gln	Asn	Ala	Ser	Gln	Val	Ser	Ile	Ser	Ile	Ser
			45					50				
Glu	His	Ser	Trp	Ile	Gly	Leu	Leu	Ser	Leu	Lys	Ser	Val
					60					65		
Glu	Arg	Ser	Asp	Ala	Gly	Leu	Tyr	Trp	Cys	Gln	Val	Lys
		70					75					80
Asp	Gly	Glu	Glu	Thr	Lys	Ile	Ser	Gln	Ser	Val	Trp	Leu
				85					90			
Thr	Val	Glu	Gly	Val	Pro	Phe	Phe	Thr	Val	Glu	Pro	Lys
	95					100					105	
Asp	Leu	Ala	Val	Pro	Pro	Asn	Ala	Pro	Phe	Gln	Leu	Ser
			110					115				
Cys	Glu	Ala	Val	Gly	Pro	Pro	Glu	Pro	Val	Thr	Ile	Tyr
					125					130		
Trp	Trp	Arg	Gly	Leu	Thr	Lys	Val	Gly	Gly	Pro	Ala	Pro
		135					140					145
Ser	Pro	Ser	Val	Leu	Asn	Val	Thr	Gly	Val	Thr	Gln	Arg
				150					155			
Thr	Glu	Phe	Ser	Cys	Glu	Ala	Arg	Asn	Ile	Lys	Gly	Leu
	160					165					170	
Ala	Thr	Ser	Arg	Pro	Ala	Ile	Val	Arg	Leu	Gln	Ala	Pro
			175					180				
Pro	Ala	Ala	Pro	Phe	Asn	Thr	Thr	Val	Thr	Thr	Ile	Ser
					190					195		
Ser	Tyr	Asn	Ala	Ser	Val	Ala	Trp	Val	Pro	Gly	Ala	Asp
		200					205					210
Gly	Leu	Ala	Leu	Leu	His	Ser	Cys	Thr	Val	Gln	Val	Ala
				215					220			
His	Ala	Pro	Gly	Glu	Trp	Glu	Ala	Leu	Ala	Val	Val	Val
	225					230					235	
Pro	Val	Pro	Pro	Phe	Thr	Cys	Leu	Leu	Arg	Asn	Leu	Ala
			240					245				
Pro	Ala	Thr	Asn	Tyr	Ser	Leu	Arg	Val	Arg	Cys	Ala	Asn
					255					260		
Ala	Leu	Gly	Pro	Ser	Pro	Tyr	Gly	Asp	Trp	Val	Pro	Phe
		265					270					275
Gln	Thr	Lys	Gly	Leu	Ala	Pro	Ala	Arg	Ala	Pro	Gln	Asn
				280					285			
Phe	His	Ala	Ile	Arg	Thr	Asp	Ser	Gly	Leu	Ile	Leu	Glu
	290					295					300	
Trp	Glu	Glu	Val	Ile	Pro	Glu	Asp	Pro	Gly	Glu	Gly	Pro
			305					310				
Leu	Gly	Pro	Tyr	Lys	Leu	Ser	Trp	Val	Gln	Glu	Asn	Gly
					320					325		
Thr	Gln	Asp	Glu	Leu	Met	Val	Glu	Gly	Thr	Arg	Ala	Asn
		330					335					340
Leu	Thr	Asp	Trp	Asp	Pro	Gln	Lys	Asp	Leu	Ile	Leu	Arg
				345					350			
Val	Cys	Ala	Ser	Asn	Ala	Ile	Gly	Asp	Gly	Pro	Trp	Ser
	355					360					365	

Gln	Pro	Leu	Val	Val	Ser	Ser	His	Asp	His	Ala	Gly	Arg
			370					375				
Gln	Gly	Pro	Pro	His	Ser	Arg	Thr	Ser	Trp	Val	Pro	Val
380					385					390		
Val	Leu	Gly	Val	Leu	Thr	Ala	Leu	Ile	Thr	Ala	Ala	Ala
		395					400					405
Leu	Ala	Leu	Ile	Leu	Leu	Arg	Lys	Arg	Arg	Lys	Glu	Thr
				410					415			
Arg	Phe	Gly	Gln	Ala	Phe	Asp	Ser	Val	Met	Ala	Arg	Gly
	420					425					430	
Glu	Pro	Ala	Val	His	Phe	Arg	Ala	Ala	Arg	Ser	Phe	Asn
			435					440				
Arg	Glu	Arg	Pro	Glu	Arg	Ile	Glu	Ala	Thr	Leu	Asp	Ser
445					450					455		
Leu	Gly	Ile	Ser	Asp	Glu	Leu	Lys	Glu	Lys	Leu	Glu	Asp
		460					465					470
Val	Leu	Ile	Pro	Glu	Gln	Gln	Phe	Thr	Leu	Gly	Arg	Met
				475					480			
Leu	Gly	Lys	Gly	Glu	Phe	Gly	Ser	Val	Arg	Glu	Ala	Gln
	485					490					495	
Leu	Lys	Gln	Glu	Asp	Gly	Ser	Phe	Val	Lys	Val	Ala	Val
			500					505				
Lys	Met	Leu	Lys	Ala	Asp	Ile	Ile	Ala	Ser	Ser	Asp	Ile
510					515					520		
Glu	Glu	Phe	Leu	Arg	Glu	Ala	Ala	Cys	Met	Lys	Glu	Phe
		525					530					535
Asp	His	Pro	His	Val	Ala	Lys	Leu	Val	Gly	Val	Ser	Leu
				540					545			
Arg	Ser	Arg	Ala	Lys	Gly	Arg	Leu	Pro	Ile	Pro	Met	Val
	550					555					560	
Ile	Leu	Pro	Phe	Met	Lys	His	Gly	Asp	Leu	His	Ala	Phe
			565					570				
Leu	Leu	Ala	Ser	Arg	Ile	Gly	Glu	Asn	Pro	Phe	Asn	Leu
575					580					585		
Pro	Leu	Gln	Thr	Leu	Val	Arg	Phe	Met	Val	Asp	Ile	Ala
		590					595					600
Cys	Gly	Met	Glu	Tyr	Leu	Ser	Ser	Arg	Asn	Phe	Ile	His
				605					610			
Arg	Asp	Leu	Ala	Ala	Arg	Asn	Cys	Met	Leu	Ala	Glu	Asp
	615					620					625	
Met	Thr	Val	Cys	Val	Ala	Asp	Phe	Gly	Leu	Ser	Arg	Lys
			630					635				
Ile	Tyr	Ser	Gly	Asp	Tyr	Tyr	Arg	Gln	Gly	Cys	Ala	Ser
640					645					650		
Lys	Leu	Pro	Val	Lys	Trp	Leu	Ala	Leu	Glu	Ser	Leu	Ala
		655					660					665
Asp	Asn	Leu	Tyr	Thr	Val	His	Ser	Asp	Val	Trp	Ala	Phe
				670					675			
Gly	Val	Thr	Met	Trp	Glu	Ile	Met	Thr	Arg	Gly	Gln	Thr
	680					685					690	
Pro	Tyr	Ala	Gly	Ile	Glu	Asn	Ala	Glu	Ile	Tyr	Asn	Tyr
			695					700				
Leu	Ile	Gly	Gly	Asn	Arg	Leu	Lys	Gln	Pro	Pro	Glu	Cys
705					710					715		
Met	Glu	Glu	Val	Tyr	Asp	Leu	Met	Tyr	Gln	Cys	Trp	Ser
		720					725					730
Ala	Asp	Pro	Lys	Gln	Arg	Pro	Ser	Phe	Thr	Cys	Leu	Arg
				735					740			
Met	Glu	Leu	Glu	Asn	Ile	Leu	Gly	His	Leu	Ser	Val	Leu
	745					750					755	
Ser	Thr	Ser	Gln	Asp	Pro	Leu	Tyr	Ile	Asn	Ile	Glu	Arg
			760					765				
Ala	Glu	Gln	Pro	Thr	Glu	Ser	Gly	Ser	Pro	Glu	Leu	His
770					775					780		
Cys	Gly	Glu	Arg	Ser	Ser	Ser	Glu	Ala	Gly	Asp	Gly	Ser
		785					790					795
Gly	Val	Gly	Ala	Val	Gly	Gly	Ile	Pro	Ser	Asp	Ser	Arg
				800						805		

Tyr	Ile	Phe	Ser	Pro	Gly	Gly	Leu	Ser	Glu	Ser	Pro	Gly
	810					815					820	
Gln	Leu	Glu	Gln	Gln	Pro	Glu	Ser	Pro	Leu	Asn	Glu	Asn
			825					830				
Gln	Arg	Leu	Leu	Leu	Leu	Gln	Gln	Gly	Leu	Leu	Pro	His
835					840					845		
Ser	Ser	Cys										
		850										

(4) INFORMATION FOR SEQUENCE ID NO. 3:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 876 AMINO ACIDS

(B) TYPE: AMINO ACID

(C) TOPOLOGY: LINEAR

(2) MOLECULE TYPE: PROTEIN

(3) SEQUENCE DESCRIPTION: SEQ ID NO. 3:

Met	Gly	Arg	Pro	Gly	Leu	Pro	Pro	Leu	Pro	Leu	Pro	Pro
1				5					10			
Pro	Pro	Arg	Leu	Gly	Leu	Leu	Leu	Ala	Glu	Ser	Ala	Ala
	15					20					25	
Ala	Gly	Leu	Lys	Leu	Met	Gly	Ala	Pro	Val	Lys	Leu	Thr
			30					35				
Val	Ser	Gln	Gly	Gln	Pro	Val	Lys	Leu	Asn	Cys	Ser	Val
40					45					50		
Glu	Gly	Met	Glu	Glu	Pro	Asp	Ile	Gln	Trp	Val	Lys	Asp
		55					60					65
Gly	Ala	Val	Val	Gln	Asn	Leu	Asp	Gln	Leu	Tyr	Ile	Pro
				70					75			
Val	Ser	Glu	Gln	His	Trp	Ile	Gly	Phe	Leu	Ser	Leu	Lys
	80					85					90	
Ser	Val	Glu	Arg	Ser	Asp	Ala	Gly	Arg	Tyr	Trp	Cys	Gln
			95					100				
Val	Glu	Asp	Gly	Gly	Glu	Thr	Glu	Ile	Ser	Gln	Pro	Val
105					110					115		
Trp	Leu	Thr	Val	Glu	Gly	Val	Pro	Phe	Phe	Thr	Val	Glu
		120				125						130
Pro	Lys	Asp	Leu	Ala	Val	Pro	Pro	Asn	Ala	Pro	Phe	Gln
				135					140			
Leu	Ser	Cys	Glu	Ala	Val	Gly	Pro	Pro	Glu	Pro	Val	Thr
	145					150					155	
Ile	Val	Trp	Trp	Arg	Gly	Thr	Thr	Lys	Ile	Gly	Gly	Pro
			160					165				
Ala	Pro	Ser	Pro	Ser	Val	Leu	Asn	Val	Thr	Gly	Val	Thr
170					175					180		
Gln	Ser	Thr	Met	Phe	Ser	Cys	Glu	Ala	His	Asn	Leu	Lys
		185				190						195
Gly	Leu	Ala	Ser	Ser	Arg	Thr	Ala	Thr	Val	His	Leu	Gln
				200					205			
Ala	Leu	Pro	Ala	Ala	Pro	Phe	Asn	Ile	Thr	Val	Thr	Lys
210						215					220	
Leu	Ser	Ser	Ser	Asn	Ala	Ser	Val	Ala	Trp	Met	Pro	Gly
			225					230				
Ala	Asp	Gly	Arg	Ala	Leu	Leu	Gln	Ser	Cys	Thr	Val	Gln
235					240					245		
Val	Thr	Gln	Ala	Pro	Gly	Gly	Trp	Glu	Val	Leu	Ala	Val
		250					255					260
Val	Val	Pro	Val	Pro	Pro	Phe	Thr	Cys	Leu	Leu	Arg	Asp
				265					270			
Leu	Val	Pro	Ala	Thr	Asn	Tyr	Ser	Leu	Arg	Val	Arg	Cys
	275					280					285	
Ala	Asn	Ala	Leu	Gly	Pro	Ser	Pro	Tyr	Ala	Asp	Trp	Val
			290					295				
Pro	Phe	Gln	Thr	Lys	Gly	Leu	Ala	Pro	Ala	Ser	Ala	Pro
300					305					310		

Gln	Asn	Leu 315	His	Ala	Ile	Arg	Thr 320	Asp	Ser	Gly	Leu	Ile 325
Leu	Glu	Trp	Glu	Glu 330	Val	Ile	Pro	Glu	Ala 335	Pro	Leu	Glu
Gly	Pro 340	Leu	Gly	Pro	Tyr	Lys 345	Leu	Ser	Trp	Val	Gln 350	Asp
Asn	Gly	Thr	Gln 355	Asp	Glu	Leu	Thr	Val 360	Glu	Gly	Thr	Arg
Ala 365	Asn	Leu	Thr	Gly	Trp 370	Asp	Pro	Gln	Lys	Asp 375	Leu	Ile
Val	Arg	Val 380	Cys	Val	Ser	Asn	Ala 385	Val	Gly	Cys	Gly	Pro 390
Trp	Ser	Gln	Pro	Leu 395	Val	Val	Ser	Ser	His 400	Asp	Arg	Ala
Gly	Gln 405	Gln	Gly	Pro	Pro	His 410	Ser	Arg	Thr	Ser	Trp 415	Val
Pro	Val	Val	Leu 420	Gly	Val	Leu	Thr	Ala 425	Leu	Val	Thr	Ala
Ala 430	Ala	Leu	Ala	Leu	Ile 435	Leu	Leu	Arg	Lys	Arg 440	Arg	Lys
Glu	Thr	Arg 445	Phe	Gly	Gln	Ala	Phe 450	Asp	Ser	Val	Met	Ala 455
Arg	Gly	Glu	Pro	Ala 460	Val	His	Phe	Arg	Ala 465	Ala	Arg	Ser
Phe	Asn 470	Arg	Glu	Arg	Pro	Glu 475	Arg	Ile	Glu	Ala	Thr 480	Leu
Asp	Ser	Leu	Gly 485	Ile	Ser	Asp	Glu	Leu	Lys	Glu	Lys	Leu
Glu 495	Asp	Val	Leu	Ile	Pro 500	Glu	Gln	Gln	Phe	Thr 505	Leu	Gly
Arg	Met	Leu 510	Gly	Lys	Gly	Glu	Phe 515	Gly	Ser	Val	Arg	Glu 520
Ala	Gln	Leu	Lys	Gln 525	Glu	Asp	Gly	Ser	Phe 530	Val	Lys	Val
Ala	Val 535	Lys	Met	Leu	Lys	Ala 540	Asp	Ile	Ile	Ala	Ser 545	Ser
Asp	Ile	Glu	Glu 550	Phe	Leu	Arg	Glu	Ala 555	Ala	Cys	Met	Lys
Glu 560	Phe	Asp	His	Pro	His 565	Val	Ala	Lys	Leu	Val 570	Gly	Val
Ser	Leu	Arg 575	Ser	Arg	Ala	Lys	Gly 580	Arg	Leu	Pro	Ile	Pro 585
Met	Val	Ile	Leu	Pro 590	Phe	Met	Lys	His	Gly 595	Asp	Leu	His
Ala	Phe 600	Leu	Leu	Ala	Ser	Arg 605	Ile	Gly	Glu	Asn	Pro 610	Phe
Asn	Leu	Pro	Leu 615	Gln	Thr	Leu	Ile	Arg 620	Phe	Met	Val	Asp
Ile 625	Ala	Cys	Gly	Met	Glu 630	Tyr	Leu	Ser	Ser	Arg 635	Asn	Phe
Ile	His	Arg 640	Asp	Leu	Ala	Ala	Arg 645	Asn	Cys	Met	Leu	Ala 650
Glu	Asp	Met	Thr	Val 655	Cys	Val	Ala	Asp	Phe 660	Gly	Leu	Ser
Arg	Lys 665	Ile	Tyr	Ser	Gly	Asp 670	Tyr	Tyr	Arg	Gln	Gly 675	Cys
Ala	Ser	Lys	Leu 680	Pro	Val	Lys	Trp	Leu 685	Ala	Leu	Glu	Ser
Leu 690	Ala	Asp	Asn	Leu	Tyr 695	Thr	Val	Gln	Ser	Asp 700	Val	Trp
Ala	Phe	Gly 705	Val	Thr	Met	Trp	Glu 710	Ile	Met	Thr	Arg	Gly 715
Gln	Thr	Pro	Tyr	Ala 720	Gly	Ile	Glu	Asn	Ala 725	Glu	Ile	Tyr
Asn	Tyr 730	Leu	Ile	Gly	Gly	Asn 735	Arg	Leu	Lys	Gln	Pro 740	Pro
Glu	Cys	Met	Glu 745	Asp	Val	Tyr	Asp	Leu 750	Met	Tyr	Gln	Cys

Trp 755	Ser	Ala	Asp	Pro	Lys 760	Gln	Arg	Pro	Ser	Phe 765	Thr	Cys
Leu	Arg	Met 770	Glu	Leu	Glu	Asn	Ile 775	Leu	Gly	Gln	Leu	Ser 780
Val	Leu	Ser	Ala	Ser 785	Gln	Asp	Pro	Leu	Tyr 790	Ile	Asn	Ile
Glu	Arg 795	Ala	Glu	Glu	Pro	Thr 800	Val	Gly	Gly	Ser	Leu 805	Glu
Leu	Pro	Gly	Arg 810	Asp	Gln	Pro	Tyr	Ser 815	Gly	Ala	Gly	Asp
Gly 820	Ser	Gly	Met	Gly	Ala 825	Val	Gly	Gly	Thr	Pro 830	Ser	Asp
Cys	Arg	Tyr 835	Ile	Leu	Thr	Pro	Gly 840	Gly	Leu	Ala	Glu	Gln 845
Pro	Gly	Gln	Ala	Glu 850	His	Gln	Pro	Glu	Ser 855	Pro	Leu	Asn
Glu	Thr 860	Gln	Arg	Leu	Leu	Leu 865	Leu	Gln	Gln	Gly	Leu 870	Leu
Pro	His	Ser	Ser 875	Cys								

(5) INFORMATION FOR SEQUENCE ID NO. 4:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 850 AMINO ACIDS

(B) TYPE: AMINO ACID

(C) TOPOLOGY: LINEAR

(2) MOLECULE TYPE: PROTEIN

(3) SEQUENCE DESCRIPTION: SEQ ID NO. 4:

Ala 1	Gly	Leu	Lys	Leu 5	Met	Gly	Ala	Pro	Val 10	Lys	Leu	Thr
Val	Ser 15	Gln	Gly	Gln	Pro	Val 20	Lys	Leu	Asn	Cys	Ser 25	Val
Glu	Gly	Met	Glu 30	Glu	Pro	Asp	Ile	Gln 35	Trp	Val	Lys	Asp
Gly 40	Ala	Val	Val	Gln	Asn 45	Leu	Asp	Gln	Leu	Tyr 50	Ile	Pro
Val	Ser	Glu 55	Gln	His	Trp	Ile	Gly 60	Phe	Leu	Ser	Leu	Lys 65
Ser	Val	Glu	Arg	Ser 70	Asp	Ala	Gly	Arg	Tyr 75	Trp	Cys	Gln
Val	Glu 80	Asp	Gly	Gly	Glu	Thr 85	Glu	Ile	Ser	Gln	Pro 90	Val
Trp	Leu	Thr 95	Val	Glu	Gly	Val	Pro	Phe 100	Phe	Thr	Val	Glu
Pro 105	Lys	Asp	Leu	Ala 110	Val	Pro	Pro	Asn	Ala	Pro 115	Phe	Gln
Leu	Ser	Cys 120	Glu	Ala	Val	Gly	Pro 125	Pro	Glu	Pro	Val	Thr 130
Ile	Val	Trp	Trp	Arg 135	Gly	Thr	Thr	Lys	Ile 140	Gly	Gly	Pro
Ala	Pro 145	Ser	Pro	Ser	Val	Leu 150	Asn	Val	Thr	Gly	Val 155	Thr
Gln	Ser	Thr	Met 160	Phe	Ser	Cys	Glu	Ala 165	His	Asn	Leu	Lys
Gly 170	Leu	Ala	Ser	Ser	Arg 175	Thr	Ala	Thr	Val	His 180	Leu	Gln
Ala	Leu	Pro 185	Ala	Ala	Pro	Phe	Asn 190	Ile	Thr	Val	Thr	Lys 195
Leu	Ser	Ser	Ser	Asn 200	Ala	Ser	Val	Ala	Trp 205	Met	Pro	Gly
Ala	Asp 210	Gly	Arg	Ala	Leu	Leu 215	Gln	Ser	Cys	Thr	Val 220	Gln
Val	Thr	Gln	Ala 225	Pro	Gly	Gly	Trp	Glu 230	Val	Leu	Ala	Val

Val 235	Val	Pro	Val	Pro	Pro 240	Phe	Thr	Cys	Leu	Leu 245	Arg	Asp
Leu	Val	Pro 250	Ala	Thr	Asn	Tyr	Ser 255	Leu	Arg	Val	Arg	Cys 260
Ala	Asn	Ala	Leu	Gly 265	Pro	Ser	Pro	Tyr	Ala 270	Asp	Trp	Val
Pro	Phe 275	Gln	Thr	Lys	Gly	Leu 280	Ala	Pro	Ala	Ser	Ala 285	Pro
Gln	Asn	Leu	His 290	Ala	Ile	Arg	Thr	Asp 295	Ser	Gly	Leu	Ile
Leu 300	Glu	Trp	Glu	Glu	Val 305	Ile	Pro	Glu	Ala	Pro 310	Leu	Glu
Gly	Pro	Leu 315	Gly	Pro	Tyr	Lys	Leu 320	Ser	Trp	Val	Gln	Asp 325
Asn	Gly	Thr	Gln	Asp 330	Glu	Leu	Thr	Val	Glu 335	Gly	Thr	Arg
Ala	Asn 340	Leu	Thr	Gly	Trp	Asp 345	Pro	Gln	Lys	Asp	Leu 350	Ile
Val	Arg	Val	Cys 355	Val	Ser	Asn	Ala	Val 360	Gly	Cys	Gly	Pro
Trp 365	Ser	Gln	Pro	Leu	Val 370	Val	Ser	Ser	His	Asp 375	Arg	Ala
Gly	Gln	Gln 380	Gly	Pro	Pro	His	Ser 385	Arg	Thr	Ser	Trp	Val 390
Pro	Val	Val	Leu	Gly 395	Val	Leu	Thr	Ala	Leu 400	Val	Thr	Ala
Ala	Ala 405	Leu	Ala	Leu	Ile	Leu 410	Leu	Arg	Lys	Arg	Arg 415	Lys
Glu	Thr	Arg	Phe 420	Gly	Gln	Ala	Phe	Asp 425	Ser	Val	Met	Ala
Arg 430	Gly	Glu	Pro	Ala	Val 435	His	Phe	Arg	Ala	Ala 440	Arg	Ser
Phe	Asn	Arg 445	Glu	Arg	Pro	Glu	Arg 450	Ile	Glu	Ala	Thr	Leu 455
Asp	Ser	Leu	Gly	Ile 460	Ser	Asp	Glu	Leu	Lys 465	Glu	Lys	Leu
Glu	Asp 470	Val	Leu	Ile	Pro	Glu 475	Gln	Gln	Phe	Thr	Leu 480	Gly
Arg	Met	Leu	Gly 485	Lys	Gly	Glu	Phe	Gly 490	Ser	Val	Arg	Glu
Ala 495	Gln	Leu	Lys	Gln	Glu 500	Asp	Gly	Ser	Phe	Val 505	Lys	Val
Ala	Val	Lys 510	Met	Leu	Lys	Ala	Asp 515	Ile	Ile	Ala	Ser	Ser 520
Asp	Ile	Glu	Glu	Phe 525	Leu	Arg	Glu	Ala	Ala 530	Cys	Met	Lys
Glu	Phe 535	Asp	His	Pro	His	Val 540	Ala	Lys	Leu	Val	Gly 545	Val
Ser	Leu	Arg	Ser 550	Arg	Ala	Lys	Gly	Arg 555	Leu	Pro	Ile	Pro
Met 560	Val	Ile	Leu	Pro	Phe 565	Met	Lys	His	Gly	Asp 570	Leu	His
Ala	Phe 575	Leu	Leu	Ala	Ser	Arg	Ile 580	Gly	Glu	Asn	Pro	Phe 585
Asn	Leu	Pro	Leu	Gln 590	Thr	Leu	Ile	Arg	Phe 595	Met	Val	Asp
Ile	Ala 600	Cys	Gly	Met	Glu	Tyr 605	Leu	Ser	Ser	Arg	Asn 610	Phe
Ile	His	Arg	Asp 615	Leu	Ala	Ala	Arg	Asn 620	Cys	Met	Leu	Ala
Glu 625	Asp	Met	Thr	Val	Cys 630	Val	Ala	Asp	Phe	Gly 635	Leu	Ser
Arg	Lys	Ile 640	Tyr	Ser	Gly	Asp	Tyr 645	Tyr	Arg	Gln	Gly	Cys 650
Ala	Ser	Lys	Leu	Pro 655	Val	Lys	Trp	Leu	Ala 660	Leu	Glu	Ser
Leu	Ala 665	Asp	Asn	Leu	Tyr	Thr 670	Val	Gln	Ser	Asp	Val 675	Trp

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Ala	Phe	Gly	Val	Thr	Met	Trp	Glu	Ile	Met	Thr	Arg	Gly
			680					685				
Gln	Thr	Pro	Tyr	Ala	Gly	Ile	Glu	Asn	Ala	Glu	Ile	Tyr
690					695					700		
Asn	Tyr	Leu	Ile	Gly	Gly	Asn	Arg	Leu	Lys	Gln	Pro	Pro
		705				710						715
Glu	Cys	Met	Glu	Asp	Val	Tyr	Asp	Leu	Met	Tyr	Gln	Cys
				720					725			
Trp	Ser	Ala	Asp	Pro	Lys	Gln	Arg	Pro	Ser	Phe	Thr	Cys
	730					735					740	
Leu	Arg	Met	Glu	Leu	Glu	Asn	Ile	Leu	Gly	Gln	Leu	Ser
			745					750				
Val	Leu	Ser	Ala	Ser	Gln	Asp	Pro	Leu	Tyr	Ile	Asn	Ile
755					760					765		
Glu	Arg	Ala	Glu	Glu	Pro	Thr	Val	Gly	Gly	Ser	Leu	Glu
		770					775					780
Leu	Pro	Gly	Arg	Asp	Gln	Pro	Tyr	Ser	Gly	Ala	Gly	Asp
				785					790			
Gly	Ser	Gly	Met	Gly	Ala	Val	Gly	Gly	Thr	Pro	Ser	Asp
	795					800					805	
Cys	Arg	Tyr	Ile	Leu	Thr	Pro	Gly	Gly	Leu	Ala	Glu	Gln
			810					815				
Pro	Gly	Gln	Ala	Glu	His	Gln	Pro	Glu	Ser	Pro	Leu	Asn
820					825					830		
Glu	Thr	Gln	Arg	Leu	Leu	Leu	Leu	Gln	Gln	Gly	Leu	Leu
		835				840						845
Pro	His	Ser	Ser	Cys								
				850								

(6) INFORMATION FOR SEQUENCE ID NO. 5:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 386 AMINO ACIDS

(B) TYPE: AMINO ACID

(C) TOPOLOGY: LINEAR

(2) MOLECULE TYPE: PROTEIN

(3) SEQUENCE DESCRIPTION: SEQ ID NO. 5:

											Ala	Gly
											1	
Leu	Lys	Leu	Met	Gly	Ala	Pro	Val	Lys	Met	Thr	Val	Ser
		5					10					15
Gln	Gly	Gln	Pro	Val	Lys	Leu	Asn	Cys	Ser	Val	Glu	Gly
				20					25			
Met	Glu	Asp	Pro	Asp	Ile	His	Trp	Met	Lys	Asp	Gly	Thr
		30				35					40	
Val	Val	Gln	Asn	Ala	Ser	Gln	Val	Ser	Ile	Ser	Ile	Ser
			45					50				
Glu	His	Ser	Trp	Ile	Gly	Leu	Leu	Ser	Leu	Lys	Ser	Val
					60					65		
Glu	Arg	Ser	Asp	Ala	Gly	Leu	Tyr	Trp	Cys	Gln	Val	Lys
		70					75					80
Asp	Gly	Glu	Glu	Thr	Lys	Ile	Ser	Gln	Ser	Val	Trp	Leu
				85					90			
Thr	Val	Glu	Gly	Val	Pro	Phe	Phe	Thr	Val	Glu	Pro	Lys
						100					105	
Asp	Leu	Ala	Val	Pro	Pro	Asn	Ala	Pro	Phe	Gln	Leu	Ser
			110					115				
Cys	Glu	Ala	Val	Gly	Pro	Pro	Glu	Pro	Val	Thr	Ile	Tyr
120					125					130		
Trp	Trp	Arg	Gly	Leu	Thr	Lys	Val	Gly	Gly	Pro	Ala	Pro
		135					140					145
Ser	Pro	Ser	Val	Leu	Asn	Val	Thr	Gly	Val	Thr	Gln	Arg
				150					155			

Thr	Glu	Phe	Ser	Cys	Glu	Ala	Arg	Asn	Ile	Lys	Gly	Leu
Ala	Thr	Ser	Arg	Pro	Ala	Ile	Val	Arg	Leu	Gln	Ala	Pro
Pro	Ala	Ala	Pro	Phe	Asn	Thr	Thr	Val	Thr	Thr	Ile	Ser
185	Ser	Tyr	Asn	Ala	Ser	Val	Ala	Trp	Val	Pro	Gly	Ala
		200					205					210
Gly	Leu	Ala	Leu	Leu	His	Ser	Cys	Thr	Val	Gln	Val	Ala
			215						220			
His	Ala	Pro	Gly	Glu	Trp	Glu	Ala	Leu	Ala	Val	Val	Val
	225					230					235	
Pro	Val	Pro	Pro	Phe	Thr	Cys	Leu	Leu	Arg	Asn	Leu	Ala
			240					245				
Pro	Ala	Thr	Asn	Tyr	Ser	Leu	Arg	Val	Arg	Cys	Ala	Asn
250	Ala	Leu	Gly	Pro	Ser	Pro	Tyr	Gly	Asp	Trp	Val	Phe
		265						270				275
Gln	Thr	Lys	Gly	Leu	Ala	Pro	Ala	Arg	Ala	Pro	Gln	Asn
				280					285			
Phe	His	Ala	Ile	Arg	Thr	Asp	Ser	Gly	Leu	Ile	Leu	Glu
	290					295					300	
Trp	Glu	Glu	Val	Ile	Pro	Glu	Asp	Pro	Gly	Glu	Gly	Pro
			305					310				
Leu	Gly	Pro	Tyr	Lys	Leu	Ser	Trp	Val	Gln	Glu	Asn	Gly
315					320					325		
Thr	Gln	Asp	Glu	Leu	Met	Val	Glu	Gly	Thr	Arg	Ala	Asn
		330					335					340
Leu	Thr	Asp	Trp	Asp	Pro	Gln	Lys	Asp	Leu	Ile	Leu	Arg
				345					350			
Val	Cys	Ala	Ser	Asn	Ala	Ile	Gly	Asp	Gly	Pro	Trp	Ser
	355					360					365	
Gln	Pro	Leu	Val	Val	Ser	Ser	His	Asp	His	Ala	Gly	Arg
			370					375				
Gln	Gly	Pro	Pro	His	Ser	Arg						
380					385							

(7) INFORMATION FOR SEQUENCE ID NO. 6:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 386 AMINO ACIDS

(B) TYPE: AMINO ACID

(C) TOPOLOGY: LINEAR

(2) MOLECULE TYPE: PROTEIN

(3) SEQUENCE DESCRIPTION: SEQ ID NO. 6:

Ala	Gly	Leu	Lys	Leu	Met	Gly	Ala	Pro	Val	Lys	Leu	Thr
1				5					10			
Val	Ser	Gln	Gly	Gln	Pro	Val	Lys	Leu	Asn	Cys	Ser	Val
	15					20				25		
Glu	Gly	Met	Glu	Glu	Pro	Asp	Ile	Gln	Trp	Val	Lys	Asp
			30					35				
Gly	Ala	Val	Val	Gln	Asn	Leu	Asp	Gln	Leu	Tyr	Ile	Pro
40					45					50		
Val	Ser	Glu	Gln	His	Trp	Ile	Gly	Phe	Leu	Ser	Leu	Lys
		55					60				65	
Ser	Val	Glu	Arg	Ser	Asp	Ala	Gly	Arg	Tyr	Trp	Cys	Gln
				70					75			
Val	Glu	Asp	Gly	Gly	Glu	Thr	Glu	Ile	Ser	Gln	Pro	Val
	80					85					90	
Trp	Leu	Thr	Val	Glu	Gly	Val	Pro	Phe	Phe	Thr	Val	Glu
			95					100				
Pro	Lys	Asp	Leu	Ala	Val	Pro	Pro	Asn	Ala	Pro	Phe	Gln
105					110					115		
Leu	Ser	Cys	Glu	Ala	Val	Gly	Pro	Pro	Glu	Pro	Val	Thr
		120					125					130

Ile	Val	Trp	Trp	Arg	Gly	Thr	Thr	Lys	Ile	Gly	Gly	Pro
Ala	Pro	Ser	Pro	Ser	Val	Leu	Asn	Val	Thr	Gly	Val	Thr
Gln	Ser	Thr	Met	Phe	Ser	Cys	Glu	Ala	His	Asn	Leu	Lys
Gly	Leu	Ala	Ser	Ser	Arg	Thr	Ala	Thr	Val	His	Leu	Gln
Ala	Leu	Pro	Ala	Ala	Pro	Phe	Asn	Ile	Thr	Val	Thr	Lys
Leu	Ser	Ser	Ser	Asn	Ala	Ser	Val	Ala	Trp	Met	Pro	Gly
Ala	Asp	Gly	Arg	Ala	Leu	Leu	Gln	Ser	Cys	Thr	Val	Gln
Val	Thr	Gln	Ala	Pro	Gly	Gly	Trp	Glu	Val	Leu	Ala	Val
Val	Val	Pro	Val	Pro	Pro	Phe	Thr	Cys	Leu	Leu	Arg	Asp
Leu	Val	Pro	Ala	Thr	Asn	Tyr	Ser	Leu	Arg	Val	Arg	Cys
Ala	Asn	Ala	Leu	Gly	Pro	Ser	Pro	Tyr	Ala	Asp	Trp	Val
Pro	Phe	Gln	Thr	Lys	Gly	Leu	Ala	Pro	Ala	Ser	Ala	Pro
Gln	Asn	Leu	His	Ala	Ile	Arg	Thr	Asp	Ser	Gly	Leu	Ile
Leu	Glu	Trp	Glu	Glu	Val	Ile	Pro	Glu	Ala	Pro	Leu	Glu
Gly	Pro	Leu	Gly	Pro	Tyr	Lys	Leu	Ser	Trp	Val	Gln	Asp
Asn	Gly	Thr	Gln	Asp	Glu	Leu	Thr	Val	Glu	Gly	Thr	Arg
Ala	Asn	Leu	Thr	Gly	Trp	Asp	Pro	Gln	Lys	Asp	Leu	Ile
Val	Arg	Val	Cys	Val	Ser	Asn	Ala	Val	Gly	Cys	Gly	Pro
Trp	Ser	Gln	Pro	Leu	Val	Val	Ser	Ser	His	Asp	Arg	Ala
Gly	Gln	Gln	Gly	Pro	Pro	His	Ser	Arg		375		
		380				385						

(8) INFORMATION FOR SEQUENCE ID NO. 7:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3919 BASE PAIRS

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

(2) MOLECULE TYPE: cDNA

(3) SEQUENCE DESCRIPTION: SEQ ID NO. 7:

GGCACGAGTG	TGGAAGGAGC	GCGGTGGCCC	AGCCGCAGCC	CCGGGGACTC	CTCGCTGCTG	60
ACGGCGGTGG	CCGCGGCTCT	AGGCGGCCGC	GGGTCCCGGA	CGCCCCGGCC	GAGCGCCGCC	120
CCCCGCCCT	CCCGCGGGCC	TCCCGCCCCT	CCTCCGCCAC	CCTCCTCTCA	GCGCTCGCGG	180
GCCGGGCCCC	GCATGGTGCG	GCGTCGCCGC	CGATGGCGCT	GAGGCGGAGC	ATGGGGTGGC	240
CGGGGCTCCG	GCCGCTGCTG	CTGGCGGGAC	TGGCTTCTCT	GCTGCTCCCC	GGGTCTGCGG	300
CCGCAGGCCT	GAAGCTCATG	GGCGCCCCAG	TGAAGATGAC	CGTGTCTCAG	GGGCAGCCAG	360
TGAAGCTCAA	CTGCAGCGTG	GAGGGGATGG	AGGACCCTGA	CATCCACTGG	ATGAAGGATG	420
GCACCGTGGT	CCAGAATGCA	AGCCAGGTGT	CCATCTCCAT	CAGCGAGCAC	AGCTGGATTG	480
GCTTACTCAG	CCTAAAGTCA	GTGGAGCGGT	CTGATGCTGG	CCTGTACTGG	TGCCAGGTGA	540

AGGATGGGGA	GGAAACCAAG	ATCTCTCAGT	CAGTATGGCT	CACTGTTCGAA	GGTGTGCCAT	600
TCTTCACAGT	GGAACCAAAA	GATCTGGCGG	TGCCACCCAA	TGCCCCTTTT	CAGCTGTCTT	660
GTGAGGCTGT	GGGTCTCCA	GAACCCGTAA	CCATTTACTG	GTGGAGAGGA	CTCACTAAAG	720
TTGGGGGACC	TGCTCCCTCT	CCCTCTGTTT	TAAATGTGAC	AGGAGTGACC	CAGCGCACAG	780
AGTTTCTCTG	TGAAGCCCGC	AACATAAAAG	GCCTGGCCAC	TTCCCGACCA	GCCATTGTTC	840
GCCTTCAAGC	ACCGCTGCA	GCTCCTTTCA	ACACCACAGT	AACAACGATC	TCCAGCTACA	900
ACGCTAGCGT	GGCCTGGGTG	CCAGGTGCTG	ACGGCCTAGC	TCTGCTGCAT	TCCTGTACTG	960
TACAGGTGGC	ACACGCCCCA	GGAGAATGGG	AGGCCCTTGC	TGTTGTGGTT	CCTGTGCCAC	1020
CTTTTACCTG	CCTGCTTCGG	AACTTGGCCC	CTGCCACCAA	CTACAGCCTT	AGGGTGCGCT	1080
GTGCCAATGC	CTTGGGCCCCT	TCTCCCTACG	GCGACTGGGT	GCCCTTTCAG	ACAAAGGGCC	1140
TAGCGCCAGC	CAGAGCTCCT	CAGAATTTCC	ATGCCATTCTG	TACCGACTCA	GGCCTTATCC	1200
TGGAATGGGA	AGAAGTGATT	CCTGAGGACC	CTGGGGAAGG	CCCCCTAGGA	CCTTATAAGC	1260
TGTCCTGGGT	CCAAGAAAAT	GGAACCCAGG	ATGAGCTGAT	GGTGAAGGG	ACCAGGGCCA	1320
ATCTGACCGA	CTGGGATCCC	CAGAAGGACC	TGATTTTTCG	TGTGTGTGCC	TCCAATGCAA	1380
TTGGTGATGG	GCCCTGGAGT	CAGCCACTGG	TGGTGTCTTC	TCATGACCAT	GCAGGGAGGC	1440
AGGGCCCTCC	CCACAGCCGC	ACATCCTGGG	TGCCTGTGGT	CCTGGGCGTG	CTCACCGCC	1500
TGATCACAGC	TGCTGCCTTG	GCCCTCATCC	TGCTTCGGAA	GAGACGCAAG	GAGACGCGTT	1560
TCGGGCAAGC	CTTTGACAGT	GTCATGGCCC	GAGGGGAGCC	AGCTGTACAC	TTCCGGGCAG	1620
CCCGATCTTT	CAATCGAGAA	AGGCCTGAAC	GCATTGAGGC	CACATTGGAT	AGCCTGGGCA	1680
TCAGCGATGA	ATTGAAGGAA	AAGCTGGAGG	ATGTCCTCAT	TCCAGAGCAG	CAGTTCACCC	1740
TCGGTCCGAT	GTTGGGCAAA	GGAGAGTTTG	GATCAGTGCG	GGAAGCCCAG	CTAAAGCAGG	1800
AAGATGGCTC	CTTCGTGAAA	GTGGCAGTGA	AGATGCTGAA	AGCTGACATC	ATTGCCTCAA	1860
GCGACATAGA	AGAGTTCCTC	CGGGAAGCAG	CTTGCATGAA	GGAGTTTGAC	CATCCACACG	1920
TGGCCAAGCT	TGTTGGGGTG	AGCCTCCGGA	GCAGGGCTAA	AGGTGCTCTC	CCCATTCCCA	1980
TGGTCATCCT	GCCCTTCATG	AAACATGGAG	ACTTGCACGC	CTTTCTGCTC	GCCTCCCGAA	2040
TCGGGGAGAA	CCCTTTTAAC	CTGCCCCCTGC	AGACCCTGGT	CCGGTTCATG	GTGGACATTG	2100
CCTGTGGCAT	GGAGTACCTG	AGCTCCCGGA	ACTTCATCCA	CCGAGACCTA	GCAGCTCGGA	2160
ATTGCATGCT	GGCCGAGGAC	ATGACAGTGT	GTGTGGCTGA	TTTTGGACTC	TCTCGGAAAA	2220
TCTATAGCGG	GGACTATTAT	CGTCAGGGCT	GTGCCTCCAA	ATTGCCCGTC	AAGTGGCTGG	2280
CCCTGGAGAG	CTTGGCTGAC	AACTTGATA	CTGTACACAG	TGATGTGTGG	GCCTTCGGGG	2340
TGACCATGTG	GGAGATCATG	ACTCGTGGGC	AGACGCCATA	TGCTGGCATT	GAAAATGCTG	2400
AGATTTACAA	CTACCTCATC	GGCGGGAACC	GCCTGAAGCA	GCCTCCGGAG	TGCATGGAGG	2460
AAGTGTATGA	TCTCATGTAC	CAGTGCTGGA	GCGCCGACCC	CAAGCAGCGC	CCAAGCTTCA	2520
CGTGTCTGCG	AATGGAACCTG	GAGAACATTC	TGGGCCACCT	GTCTGTGCTG	TCCACCAGCC	2580
AGGACCCCTT	GTACATCAAC	ATTGAGAGAG	CTGAGCAGCC	TACTGAGAGT	GGCAGCCCTG	2640
AGCTGCACTG	TGGAGAGCGA	TCCAGCAGCG	AGGCAGGGGA	CGGCAGTGGC	GTGGGGGCAG	2700
TAGGTGGCAT	CCCCAGTGAC	TCTCGGTACA	TCTTCAGCCC	CGGAGGGCTA	TCCGAGTCAC	2760
CAGGGCAGCT	GGAGCAGCAG	CCAGAAAGCC	CCCTCAATGA	GAACCAGAGG	CTGTTGTTGC	2820
TGCAGCAAGG	GCTACTGCCT	CACAGTAGCT	GTTAACCCTC	AGGCAGAGGA	AAGTTGGGGC	2880
CCCTGGCTCT	GCTGACCACT	GTGCTGCCTG	ACTAGGCCCA	GTCTGATCAC	AGCCCAGGCA	2940
GCAAGGTATG	GAGGCTCCTG	TGGTAGCCCT	CCCAAGCTGT	GCTGGCGCCT	GGACGGACCA	3000
AATTGCCCAA	TCCCAGTTCT	TCCTGCAGCC	GCTCTGGCCA	GCCTGGCATC	AGTTCAGGCC	3060
TTGGCTTAGA	GGAGGTGAGC	CAGAGCTGGT	TGCCTGAATG	CAGGCAGCTG	GCAGGAGGGG	3120
AGGGTGGCTA	TGTTTCCATG	GGTACCATGG	GTGTGGATGG	CAGTAAGGGA	GGGTAGCAAC	3180
AGCCCTGTGG	GCCCCTACCC	TCCTGGCTGA	GCTGCTCCTA	CTTTAGTGCA	TGCTTGAGAC	3240
CGCCTGCAGC	CTGGAACTCA	GCACTGCCCA	CCACACTTGG	GCCGAAATGC	CAGGTTTGCC	3300

CCTCTTAAGT	CACAAAGAGA	TGTCCATGTA	TTGTTCCCTT	TTAGGTGATG	ATTAGGAAGG	3360
GATTGGCACA	CTTGGGTCCC	TAAGCCCTAT	GGCAGGAAAT	GGTGGGATAT	TCTCAGGTCT	3420
GAATCCTCAT	CATCTTCCTG	ATTCCCCACC	CTGCAAAGGC	CTGGAAGTGG	CTGTGGGGCT	3480
CTGAGGCATG	CTGAAGGACA	AAAGATTACA	GAGATCCGAC	TTCAAAAGGC	AGGGTCTGAG	3540
TCTGGCAGGT	GGAGAGGTGC	TAAGGGGCTG	GCCCAGGAGT	CAGGCATTTT	AGGACCCCTC	3600
CAAGCTTCTA	CAGTCTGTCT	GAGCATGCTA	CCAAGCCCCC	AGATACCCCA	AAACTAACAG	3660
AGGCAGTTTT	GTCTGAGCCC	AGCCCTCCCA	CATGATGACC	CTTAGGTCTA	CCCTCCTCTC	3720
TAAATGGACA	TCCTCGTTTG	TCCCAAGTCT	CCAGAGAGAC	TACTGATGGC	TGATGTGGGT	3780
AAGAAAAGTT	CCAGGAACCA	GGGCTGGGGT	GGAACCAGGG	CTGGGGTCGA	GGCAGGCTCT	3840
TGGGCAGGCT	CTTGCTGTTA	GGAACATTTT	TAAGCTATTA	AGTTGCTGTT	TCAAAACAAA	3900
TAAAATTGAA	ACATAAAGA					3919

(9) INFORMATION FOR SEQUENCE ID NO. 8:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2550 BASE PAIRS
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(2) MOLECULE TYPE: cDNA

(3) SEQUENCE DESCRIPTION: SEQ ID NO. 8:

GCAGGCCTGA	AGCTCATGGG	CGCCCCAGTG	AAGATGACCG	TGTCTCAGGG	GCAGCCAGTG	60
AAGCTCAACT	GCAGCGTGGA	GGGGATGGAG	GACCCTGACA	TCCACTGGAT	GAAGGATGGC	120
ACCGTGGTCC	AGAATGCAAG	CCAGGTGTCC	ATCTCCATCA	GCGAGCACAG	CTGGATTGGC	180
TTACTCAGCC	TAAAGTCAGT	GGAGCGGTCT	GATGCTGGCC	TGTACTGGTG	CCAGGTGAAG	240
GATGGGGAGG	AAACCAAGAT	CTCTCAGTCA	GTATGGCTCA	CTGTGCAAGG	TGTGCCATTC	300
TTCACAGTGG	AACCAAAAGA	TCTGGCGGTG	CCACCCAATG	CCCCTTTTCA	GCTGTCTTGT	360
GAGGCTGTGG	GTCCTCCAGA	ACCCGTAACC	ATTTACTGGT	GGAGAGGACT	CACTAAAGTT	420
GGGGGACCTG	CTCCCTCTCC	CTCTGTTTTA	AATGTGACAG	GAGTGACCCA	GCGCACAGAG	480
TTTTCTTGTG	AAGCCCGCAA	CATAAAAGGC	CTGGCCACTT	CCCGACCAGC	CATTGTTTCG	540
CTTCAAGCAC	CGCCTGCAGC	TCCTTTCAAC	ACCACAGTAA	CAACGATCTC	CAGCTACAAC	600
GCTAGCGTGG	CCTGGGTGCC	AGGTGCTGAC	GGCCTAGCTC	TGCTGCATTC	CTGTACTGTA	660
CAGGTGGCAC	ACGCCCGCAG	AGAATGGGAG	GCCCTTGCTG	TTGTGGTTCC	TGTGCCACCT	720
TTTACCTGCC	TGCTTCGGAA	CTTGGCCCCC	GCCACCAACT	ACAGCCTTAG	GGTGCGCTGT	780
GCCAATGCCT	TGGGCCCTTC	TCCCTACGGC	GACTGGGTGC	CCTTTCAGAC	AAAGGGCCTA	840
GCGCCAGCCA	GAGCTCCTCA	GAATTTCCAT	GCCATTCGTA	CCGACTCAGG	CCTTATCCTG	900
GAATGGGAAG	AAGTGATTCC	TGAGGACCCT	GGGGAAGGCC	CCCTAGGACC	TTATAAGCTG	960
TCCTGGGTCC	AAGAAAATGG	AACCCAGGAT	GAGCTGATGG	TGGAAGGGAC	CAGGGCCAAT	1020
CTGACCGACT	GGGATCCCCA	GAAGGACCTG	ATTTTGCGTG	TGTGTGCCTC	CAATGCAATT	1080
GGTGATGGGC	CCTGGAGTCA	GCCACTGGTG	GTGTCTTCTC	ATGACCATGC	AGGGAGGCAG	1140
GGCCCTCCCC	ACAGCCGCAC	ATCCTGGGTG	CCTGTGGTCC	TGGGCGTGCT	CACCGCCCTG	1200
ATCACAGCTG	CTGCCTTGGC	CCTCATCCTG	CTTCGGAAGA	GACGCAAGGA	GACGCGTTTC	1260
GGGCAAGCCT	TTGACAGTGT	CATGGCCCGA	GGGGAGCCAG	CTGTACACTT	CCGGGCAGCC	1320
CGATCTTTCA	ATCGAGAAAG	GCCTGAACGC	ATTGAGGCCA	CATTGGATAG	CCTGGGCATC	1380
AGCGATGAAT	TGAAGGAAAA	GCTGGAGGAT	GTCCTCATTC	CAGAGCAGCA	GTTACCCCTC	1440

GGTCGGATGT	TGGGCAAAGG	AGAGTTTGA	TCAGTGC	AAGCCCAGCT	AAAGCAGGAA	1500
GATGGCTCCT	TCGTGAAAGT	GGCAGTGAAG	ATGCTGAAAG	CTGACATCAT	TGCCTCAAGC	1560
GACATAGAAG	AGTTCCTCCG	GGAAGCAGCT	TGCATGAAGG	AGTTTGACCA	TCCACACGTG	1620
GCCAAGCTTG	TTGGGGTGAG	CCTCCGAGC	AGGGCTAAAG	GTCGTCTCCC	CATTCCCATG	1680
GTCATCCTGC	CCTTCATGAA	ACATGGAGAC	TTGCACGCCT	TTCTGCTCGC	CTCCCCGAATC	1740
GGGGAGAACC	CTTTTAACCT	GCCCCGAGC	ACCCTGGTCC	GGTTCATGGT	GGACATTGCC	1800
TGTGGCATGG	AGTACCTGAG	CTCCCCGAAC	TTCATCCACC	GAGACCTAGC	AGCTCGGAAT	1860
TGCATGCTGG	CCGAGGACAT	GACAGTGTGT	GTGGCTGATT	TTGGACTCTC	TCGGAAAATC	1920
TATAGCGGGG	ACTATTATCG	TCAGGGCTGT	GCCTCCAAAT	TGCCCCGTCAA	GTGGCTGGCC	1980
CTGGAGAGCT	TGGCTGACAA	CTTGATACT	GTACACAGTG	ATGTGTGGGC	CTTCGGGGTG	2040
ACCATGTGGG	AGATCATGAC	TCGTGGGCAG	ACGCCATATG	CTGGCATTGA	AAATGCTGAG	2100
ATTTACAAC	ACCTCATCGG	CGGGAACCGC	CTGAAGCAGC	CTCCGGAGTG	CATGGAGGAA	2160
GTGTATGATC	TCATGTACCA	GTGCTGGAGC	GCCGACCCCA	AGCAGCGCCC	AAGCTTCACG	2220
TGTCTGCGAA	TGGAAC	TGGAAC	TGGAAC	TGGAAC	TGGAAC	2280
GACCCCTTGT	ACATCAACAT	TGAGAGAGCT	GAGCAGCCTA	CTGAGAGTGG	CAGCCCTGAG	2340
CTGCACTGTG	GAGAGCGATC	CAGCAGCGAG	GCAGGGGACG	GCAGTGGCGT	GGGGGCAGTA	2400
GGTGGCATCC	CCAGTGACTC	TCGGTACATC	TTCAGCCCCG	GAGGGCTATC	CGAGTCACCA	2460
GGGCAGCTGG	AGCAGCAGCC	AGAAAGCCCC	CTCAATGAGA	ACCAGAGGCT	GTTGTTGCTG	2520
CAGCAAGGGC	TACTGCCTCA	CAGTAGCTGT				2550

(10) INFORMATION FOR SEQUENCE ID NO. 9:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4364 BASE PAIRS
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(2) MOLECULE TYPE: cDNA

(3) SEQUENCE DESCRIPTION: SEQ ID NO. 9:

CATTAGATCT	TTACATGAAA	GTAAAATTTA	TAAGATTTCT	AGAAAGTCAA	AAGATGATAA	60
CTATTTCTTA	GGATACTAAA	AGCACTCACA	TTATAGAAAA	AAAATCAGTT	AACTATACTC	120
CACAAACATT	AAAGGCTCCC	TATAAAAAAA	CATTTTAAAT	AGGCAAGCCA	CAGAAAGGGC	180
AAATATTAAT	AGTTTGCAAT	ACATATGTAT	GAAAAGGAAT	TGAATCTAGA	ATATTTAACA	240
AAGCTTTACA	ACTCAAAAAA	TACAAAGAAA	ATATTTTCT	TCCAATTGGC	AAATTACTTA	300
AACAGAACCT	TCACAAAAGA	AGATAAGAAT	GTTTAATAAA	CATTTGAAGC	CATAATAATG	360
ACATCATTAG	CCATGATGGA	AATGCAAAT	TAAGTACCAC	TTCACATCCA	CAAGAAAAAG	420
ATAAAAATAA	AAGGACTGAG	CTCACCACAA	ATTGGTGAGG	ATGTGGTAAT	ACTGAAATTC	480
TTGTACCGTG	CTCCTGAGGG	TATAACATAT	TACAGGATTT	TTTTGAAAAC	TAGTGGTTCC	540
TTATAAACTT	AATGCCCTGG	CAACCTCACA	CCTATTTACT	TAAGAATGAA	AGGGCCCCGC	600
CCTCCTCCCT	CCTCGCTCGC	GGCCCCGGCC	CGGCATGGTG	CGGCGTCGCC	GCCGATGGCG	660
CTGAGGCGGA	GATGGGGCG	GCCGGGGCTC	CCGCCGCTGC	CGCTGCCGCC	GCCACCGCGG	720
CTCGGGCTGC	TGCTGGCGGA	GTCCGCCGCC	GCAGGTCTGA	AGCTCATGGG	AGCCCCGGTG	780
AAGCTGACAG	TGTCTCAGGG	GCAGCCGGTG	AAGCTCAACT	GCAGTGTGGA	GGGGATGGAG	840
GAGCCTGACA	TCCAGTGGGT	GAAGGATGGG	GCTGTGGTCC	AGAACTTGGA	CCAGTTGTAC	900
ATCCCAGTCA	GCGAGCAGCA	CTGGATCGGC	TTCCTCAGCC	TGAAGTCAGT	GGAGCGCTCT	960

GACGCCGGCC	GGTACTGGTG	CCAGGTGGAG	GATGGGGGTG	AAACCGAGAT	CTCCCAGCCA	1020
GTGTGGCTCA	CGGTAGAAGG	TGTGCCATTT	TTCACAGTGG	AGCCAAAAGA	TCTGGCAGTG	1080
CCACCCAATG	CCCCTTTCCA	ACTGTCTTGT	GA TGTGTGG	GTCCTCTTGA	ACCTGTTACC	1140
ATTGTCTGGT	GGAGAGGAAC	TACGAAGATC	GGGGGACCCG	CTCCCTCTCC	ATCTGTTTTA	1200
AATGTAACAG	GGGTGACCCA	GAGCACCATG	TTTTCCTGTG	AAGCTCACAA	CCTAAAAGGC	1260
CTGGCCTCTT	CTCGCACAGC	CACTGTTTAC	CTTCAAGCAC	TGCCTGCAGC	CCCCTTCAAC	1320
ATCACCGTGA	CAAAGCTTTC	CAGCAGCAAC	GCTAGTGTGG	CCTGGATGCC	AGGTGCTGAT	1380
GGCCGAGCTC	TGCTACAGTC	CTGTACAGTT	CAGGTGACAC	AGGCCCCAGG	AGGCTGGGAA	1440
GTCCTGGCTG	TTGTGGTCCC	TGTGCCCCCC	TTTACCTGCC	TGCTCCGGGA	CCTGGTGCCT	1500
GCCACCAACT	ACAGCCTCAG	GGTGCCTGTG	GCCAATGCCT	TGGGGCCCTC	TCCCTATGCT	1560
GACTGGGTGC	CCTTTCAGAC	CAAGGGTCTA	GCCCCAGCCA	GCGCTCCCCA	AAACCTCCAT	1620
GCCATCCGCA	CAGATTCAGG	CCTCATCTTG	GAGTGGGAAG	AAGTGATCCC	CGAGGCCCCCT	1680
TTGGAAGGCC	CCCTGGGACC	CTACAAACTG	TCCTGGGTTC	AAGACAATGG	AACCCAGGAT	1740
GAGCTGACAG	TGGAGGGGAC	CAGGGCCAAT	TTGACAGGCT	GGGATCCCCA	AAAGGACCTG	1800
ATCGTACGTG	TGTGCGTCTC	CAATGCAGTT	GGCTGTGGAC	CCTGGAGTCA	GCCACTGGTG	1860
GTCTCTTCTC	ATGACCGTGC	AGGCCAGCAG	GGCCCTCCTC	ACAGCCGCAC	ATCCTGGGTA	1920
CCTGTGGTCC	TTGGTGTGCT	AACGGCCCTG	GTGACGGCTG	CTGCCCTGGC	CCTCATCCTG	1980
CTTCGAAAGA	GACGGAAAGA	GACGCGGTTT	GGGCAAGCCT	TTGACAGTGT	CATGGCCCCG	2040
GGAGAGCCAG	CCGTTCACTT	CCGGGCAGCC	CGGTCTTTCA	ATCGAGAAAG	GCCCCAGCGC	2100
ATCGAGGCCA	CATTGGACAG	CTTGGGCATC	AGCGATGAAC	TAAAGGAAAA	ACTGGAGGAT	2160
GTGCTCATCC	CAGAGCAGCA	GTTCAACCCTG	GGCCGGATGT	TGGGCAAAGG	AGAGTTTGGT	2220
TCAGTGCGGG	AGGCCCAGCT	GAAGCAAGAG	GATGGCTCCT	TTGTGAAAGT	GGCTGTGAAG	2280
ATGCTGAAAG	CTGACATCAT	TGCCTCAAGC	GACATTGAAG	AGTTCCTCAG	GGAAGCAGCT	2340
TGCATGAAGG	AGTTTGACCA	TCCACACGTG	GCCAAACTTG	TTGGGGTAAG	CCTCCGGAGC	2400
AGGGCTAAAG	GCCGTCTCCC	CATCCCCATG	GTCATCTTGC	CCTTCATGAA	GCATGGGGAC	2460
CTGCATGCCT	TCCTGCTCGC	CTCCCGGATT	GGGGAGAACC	CCTTTAACCT	ACCCCTCCAG	2520
ACCCTGATCC	GGTTCATGGT	GGACATTGCC	TGCGGCATGG	AGTACCTGAG	CTCTCGGAAC	2580
TTCATCCACC	GAGACCTGGC	TGCTCGGAAT	TGCATGCTGG	CAGAGGACAT	GACAGTGTGT	2640
GTGGCTGACT	TCGGACTCTC	CCGGAAGATC	TACAGTGGGG	ACTACTATCG	TCAAGGCTGT	2700
GCCTCCAAAC	TGCCTGTCAA	GTGGCTGGCC	CTGGAGAGCC	TGGCCGACAA	CCTGTATACT	2760
GTGCAGAGTG	ACGTGTGGGC	GTTCCGGGTG	ACCATGTGGG	AGATCATGAC	ACGTGGGCAG	2820
ACGCCATATG	CTGGCATCGA	AAACGCTGAG	ATTTACAAC	ACCTCATTGG	CGGGAACCGC	2880
CTGAAACAGC	CTCCGGAGTG	TATGGAGGAC	GTGTATGATC	TCATGTACCA	GTGCTGGAGT	2940
GCTGACCCCA	AGCAGCGCCC	GAGCTTTACT	TGTCTGCGAA	TGGAACCTGA	GAACATCTTG	3000
GGCCAGCTGT	CTGTGCTATC	TGCCAGCCAG	GACCCCTTAT	ACATCAACAT	CGAGAGAGCT	3060
GAGGAGCCCA	CTGTGGGAGG	CAGCCTGGAG	CTACCTGGCA	GGGATCAGCC	CTACAGTGGG	3120
GCTGGGGATG	GCAGTGGCAT	GGGGGCAGTG	GGTGGCACTC	CCAGTGAAGT	TCGGTACATA	3180
CTCACCCCCG	GAGGGCTGGC	TGAGCAGCCA	GGGCAGGCAG	AGCACCAGCC	AGAGAGTCCC	3240
CTCAATGAGA	CACAGAGGCT	TTTGCTGCTG	CAGCAAGGGC	TACTGCCACA	CAGTAGCTGT	3300
TAGCCACAG	GCAGAGGGCA	TCGGGGCCAT	TTGGCCGGCT	CTGGTGGCCA	CTGAGCTGGC	3360
TGACTAAGCC	CCGTCTGACC	CCAGCCGAGA	CAGCAAGGTG	TGGAGGCTCC	TGTGGTAGTC	3420
CTCCCAAGCT	GTGCTGGGAA	GCCCCGACTG	ACCAAATCAC	CCAATCCCAG	TTCTTCCTGC	3480
AACCACTCTG	TGGCCAGCCT	GGCATCAGTT	TAGGCCTTGG	CTTGATGGAA	GTGGGCCAGT	3540
CCTGGTTGTC	TGAACCCAGG	CAGCTGGCAG	GAGTGGGGTG	GTTATGTTTC	CATGGTTACC	3600
ATGGGTGTGG	ATGGCAGTGT	GGGGAGGGCA	GGTCCAGCTC	TGTGGGCCCT	ACCCTCCTGC	3660
TGAGCTGCCC	CTGCTGCTTA	AGTGCATGCA	TTGAGCTGCC	TCCAGCCTGG	TGGCCCAGCT	3720

ATTACCACAC	TTGGGGTTTA	AATATCCAGG	TGTGCCCCTC	CAAGTCAGAA	AGAGATGTCC	3780
TTGTAATATT	CCCTTTTAGG	TGAGGGTTGG	TAAGGGGTTG	GTATCTCAGG	TCTGAATCTT	3840
CACCATCTTT	CTGATTCCGC	ACCCTGCCTA	CGCCAGGAGA	AGTTGAGGGG	AGCATGCTTC	3900
CCTGCAGCTG	ACCGGGTCAC	ACAAAGGCAT	GCTGGAGTAC	CCAGCCTATC	AGGTGCCCCT	3960
CTTCCAAAGG	CAGCGTGCCG	AGCCAGCAAG	AGGAAGGGGT	GCTGTGAGGC	TTGCCCAGGA	4020
GCAAGTGAGG	CCGGAGAGGA	GTTCAGGAAC	CCTTCTCCAT	ACCCACAATC	TGAGCACGCT	4080
ACCAAATCTC	AAAATATCCT	AAGACTAACA	AAGGCAGCTG	TGTCTGAGCC	CAACCCCTTCT	4140
AAACGGTGAC	CTTTAGTGCC	AACTTCCCCT	CTAACTGGAC	AGCCTCTTCT	GTCCCAAGTC	4200
TCCAGAGAGA	AATCAGGCCT	GATGAGGGGG	AATTCTTGGA	ACCTGGACCC	CAGCCTTGGT	4260
GGGGGAGCCT	CTGGAATGCA	TGGGGCGGGT	CCTAGCTGTT	AGGGACATTT	CCAAGCTGTT	4320
AGTTGCTGTT	TAAATAGAA	ATAAAATTGA	AGACTAAAGA	CCTA		4364

(11) INFORMATION FOR SEQUENCE ID NO. 10:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2550 BASE PAIRS
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(2) MOLECULE TYPE: cDNA

(3) SEQUENCE DESCRIPTION: SEQ ID NO. 10:

GCAGGTCTGA	AGCTCATGGG	AGCCCCGGTG	AAGCTGACAG	TGTCTCAGGG	GCAGCCGGTG	60
AAGCTCAACT	GCAGTGTGGA	GGGGATGGAG	GAGCCTGACA	TCCAGTGGGT	GAAGGATGGG	120
GCTGTGGTCC	AGAACTTGGA	CCAGTTGTAC	ATCCCACTCA	GCGAGCAGCA	CTGGATCGGC	180
TTCCTCAGCC	TGAAGTCAGT	GGAGCGCTCT	GACGCCGGCC	GGTACTGGTG	CCAGGTGGAG	240
GATGGGGGTG	AAACCGAGAT	CTCCCAGCCA	GTGTGGCTCA	CGGTAGAAGG	TGTGCCATTT	300
TTCACAGTGG	AGCCAAAAGA	TCTGGCAGTG	CCACCCAATG	CCCCTTTCCA	ACTGTCTTGT	360
GAGGCTGTGG	GTCCCCCTGA	ACCTGTTACC	ATTGTCTGGT	GGAGAGGAAC	TACGAAGATC	420
GGGGGACCCG	CTCCCTCTCC	ATCTGTTTTA	AATGTAACAG	GGGTGACCCA	GAGCACCATG	480
TTTTCCTGTG	AAGCTCACAA	CCTAAAAGGC	CTGGCCTCTT	CTCGCACAGC	CACTGTTTAC	540
CTTCAAGCAC	TGCCTGCAGC	CCCCTTCAAC	ATCACCGTGA	CAAAGCTTTC	CAGCAGCAAC	600
GCTAGTGTGG	CCTGGATGCC	AGGTGCTGAT	GGCCGAGCTC	TGCTACAGTC	CTGTACAGTT	660
CAGGTGACAC	AGGCCCCAGG	AGGCTGGGAA	GTCCTGGCTG	TTGTGGTCCC	TGTGCCCCCC	720
TTTACCTGCC	TGCTCCGGGA	CCTGGTGCCT	GCCACCAACT	ACAGCCTCAG	GGTGCCTGT	780
GCCAATGCCT	TGGGGCCCTC	TCCCTATGCT	GACTGGGTGC	CCTTTCAGAC	CAAGGGTCTA	840
GCCCCAGCCA	GCGCTCCCCA	AAACCTCCAT	GCCATCCGCA	CAGATTTCAGG	CCTCATCTTG	900
GAGTGGGAAG	AAGTGATCCC	CGAGGCCCCCT	TTGGAAGGCC	CCCTGGGACC	CTACAACTG	960
TCCTGGGTTC	AAGACAATGG	AACCCAGGAT	GAGCTGACAG	TGGAGGGGAC	CAGGGCCAAT	1020
TTGACAGGCT	GGGATCCCCA	AAAGGACCTG	ATCGTACGTG	TGTGCGTCTC	CAATGCAGTT	1080
GGCTGTGGAC	CCTGGAGTCA	GCCACTGGTG	GTCTCTTCTC	ATGACCGTGC	AGGCCAGCAG	1140
GGCCCTCCTC	ACAGCCGCAC	ATCCTGGGTA	CCTGTGGTCC	TTGGTGTGCT	AACGGCCCTG	1200
GTGACGGCTG	CTGCCCTGGC	CCTCATCCTG	CTTCGAAAGA	GACGGAAAGA	GACGCGGTTT	1260
GGGCAAGCCT	TTGACAGTGT	CATGGCCCCG	GGAGAGCCAG	CCGTTCACCT	CCGGGCAGCC	1320
CGGTCCTTCA	ATCGAGAAAG	GCCCGAGCGC	ATCGAGGCCA	CATTGGACAG	CTTGGGCATC	1380
AGCGATGAAC	TAAAGGAAAA	ACTGGAGGAT	GTGCTCATCC	CAGAGCAGCA	GTTACCCCTG	1440

GGCCGGATGT	TGGGCAAAGG	AGAGTTTGGT	TCAGTGCGGG	AGGCCCAGCT	GAAGCAAGAG	1500
GATGGCTCCT	TTGTGAAAGT	GGCTGTGAAG	ATGCTGAAAG	CTGACATCAT	TGCCTCAAGC	1560
GACATTGAAG	AGTTCCTCAG	GGAAGCAGCT	TGCATGAAGG	AGTTTGACCA	TCCACACGTG	1620
GCCAAACTTG	TTGGGGTAAG	CCTCCGGAGC	AGGGCTAAAG	GCCGTCTCCC	CATCCCCATG	1680
GTCATCTTGC	CCTTCATGAA	GCATGGGGAC	CTGCATGCCT	TCCTGCTCGC	CTCCCGGATT	1740
GGGGAGAACC	CCTTTAACCT	ACCCCTCCAG	ACCCTGATCC	GGTTCATGGT	GGACATTGCC	1800
TGCGGCATGG	AGTACCTGAG	CTCTCGGAAC	TTCATCCACC	GAGACCTGGC	TGCTCGGAAT	1860
TGCATGCTGG	CAGAGGACAT	GACAGTGTGT	GTGGCTGACT	TCGGACTCTC	CCGGAAGATC	1920
TACAGTGGGG	ACTACTATCG	TCAAGGCTGT	GCCTCCAAAC	TGCCTGTCAA	GTGGCTGGCC	1980
CTGGAGAGCC	TGGCCGACAA	CCTGTATACT	GTGCAGAGTG	ACGTGTGGGC	GTTCCGGGGTG	2040
ACCATGTGGG	AGATCATGAC	ACGTGGGCAG	ACGCCATATG	CTGGCATCGA	AAACGCTGAG	2100
ATTTACAAC	ACCTCATTGG	CGGGAACCGC	CTGAAACAGC	CTCCGGAGTG	TATGGAGGAC	2160
GTGTATGATC	TCATGTACCA	GTGCTGGAGT	GCTGACCCCA	AGCAGCGCCC	GAGCTTTACT	2220
TGTCTGCGAA	TGGAAC	TGGA	GAACATCTTG	GGCCAGCTGT	CTGTGCTATC	2280
GACCCCTTAT	ACATCAACAT	CGAGAGAGCT	GAGGAGCCCA	CTGTGGGAGG	CAGCCTGGAG	2340
CTACCTGGCA	GGGATCAGCC	CTACAGTGGG	GCTGGGGATG	GCAGTGGCAT	GGGGGCAGTG	2400
GGTGGCACTC	CCAGTGA	CTG	TCCGTTACATA	CTCACC	CCCCCG	2460
GGGCAGGCAG	AGCACCAGCC	AGAGAGTCCC	CTCAATGAGA	CACAGAGGCT	TTTGCTGCTG	2520
CAGCAAGGGC	TACTGCCACA	CAGTAGCTGT				2550

(12) INFORMATION FOR SEQUENCE ID NO. 11:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1158 BASE PAIRS
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(2) MOLECULE TYPE: cDNA

(3) SEQUENCE DESCRIPTION: SEQ ID NO. 11:

GCAGGCCTGA	AGCTCATGGG	CGCCCCAGTG	AAGATGACCG	TGTCTCAGGG	GCAGCCAGTG	60
AAGCTCAACT	GCAGCGTGGA	GGGGATGGAG	GACCCTGACA	TCCACTGGAT	GAAGGATGGC	120
ACCGTGGTCC	AGAATGCAAG	CCAGGTGTCC	ATCTCCATCA	GCGAGCACAG	CTGGATTGGC	180
TTACTCAGCC	TAAAGTCAGT	GGAGCGGTCT	GATGCTGGCC	TGTACTGGTG	CCAGGTGAAG	240
GATGGGGAGG	AAACCAAGAT	CTCTCAGTCA	GTATGGCTCA	CTGTCTGAAGG	TGTGCCATTG	300
TTCACAGTGG	AACCAAAAGA	TCTGGCGGTG	CCACCCAATG	CCCCTTTTCA	GCTGTCTTGT	360
GAGGCTGTGG	GTCCTCCAGA	ACCCGTAACC	ATTTACTGGT	GGAGAGGACT	CACTAAAGTT	420
GGGGGACCTG	CTCCCTCTCC	CTCTGTTTTA	AATGTGACAG	GAGTGACCCA	GCGCACAGAG	480
TTTTCTTGTG	AAGCCCGCAA	CATAAAAGGC	CTGGCCACTT	CCCGACCAGC	CATTGTTCCG	540
CTTCAAGCAC	CGCCTGCAGC	TCCTTTCAAC	ACCACAGTAA	CAACGATCTC	CAGCTACAAC	600
GCTAGCGTGG	CCTGGGTGCC	AGGTGCTGAC	GGCCTAGCTC	TGCTGCATTG	CTGTACTGTA	660
CAGGTGGCAC	ACGCCCCAGG	AGAATGGGAG	GCCCTTGCTG	TTGTGGTTCC	TGTGCCACCT	720
TTTACCTGCC	TGCTTCGGAA	CTTGGCCCCCT	GCCACCAACT	ACAGCCTTAG	GGTGCCTGTG	780
GCCAATGCCT	TGGGCCCTTC	TCCCTACGGC	GACTGGGTGC	CCTTTCAGAC	AAAGGGCCTA	840
GCGCCAGCCA	GAGCTCCTCA	GAATTTCAT	GCCATTCGTA	CCGACTCAGG	CCTTATCCTG	900
GAATGGGAAG	AAGTGATTCC	TGAGGACCCT	GGGGAAGGCC	CCCTAGGACC	TTATAAGCTG	960

TCCTGGGTCC	AAGAAAATGG	AACCCAGGAT	GAGCTGATGG	TGGAAGGGAC	CAGGGCCAAT	1020
CTGACCGACT	GGGATCCCCA	GAAGGACCTG	ATTTTGGCTG	TGTGTGCCTC	CAATGCAATT	1080
GGTGATGGGC	CCTGGAGTCA	GCCACTGGTG	GTGTCTTCTC	ATGACCATGC	AGGGAGGCAG	1140
GGCCCTCCCC	ACAGCCGC					1158

(13) INFORMATION FOR SEQUENCE ID NO. 12:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1158 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (2) MOLECULE TYPE: cDNA
- (3) SEQUENCE DESCRIPTION: SEQ ID NO. 12:

GCAGGTCTGA	AGCTCATGGG	AGCCCCGGTG	AAGCTGACAG	TGTCTCAGGG	GCAGCCGGTG	60
AAGCTCAACT	GCAGTGTGGA	GGGGATGGAG	GAGCCTGACA	TCCAGTGGGT	GAAGGATGGG	120
GCTGTGGTCC	AGAACTTGGA	CCAGTTGTAC	ATCCCAGTCA	GCGAGCAGCA	CTGGATCGGC	180
TTCTCAGCC	TGAAGTCAGT	GGAGCGCTCT	GACGCCGGCC	GGTACTGGTG	CCAGGTGGAG	240
GATGGGGGTG	AAACCGAGAT	CTCCCAGCCA	GTGTGGCTCA	CGGTAGAAGG	TGTGCCATTT	300
TTACAGTGG	AGCCAAAAGA	TCTGGCAGTG	CCACCCAATG	CCCCTTTCCA	ACTGTCTTGT	360
GAGGCTGTGG	GTCCCCCTGA	ACCTGTTACC	ATTGTCTGGT	GGAGAGGAAC	TACGAAGATC	420
GGGGGACCCG	CTCCCTCTCC	ATCTGTTTTA	AATGTAACAG	GGGTGACCCA	GAGCACCATG	480
TTTTCTGTG	AAGCTCACAA	CCTAAAAGGC	CTGGCCTCTT	CTCGCACAGC	CACTGTTCAC	540
CTTCAAGCAC	TGCCTGCAGC	CCCCTTCAAC	ATCACCGTGA	CAAAGCTTTC	CAGCAGCAAC	600
GCTAGTGTGG	CCTGGATGCC	AGGTGCTGAT	GGCCGAGCTC	TGCTACAGTC	CTGTACAGTT	660
CAGGTGACAC	AGGCCCCAGG	AGGCTGGGAA	GTCCTGGCTG	TTGTGGTCCC	TGTGCCCCCC	720
TTTACCTGCC	TGCTCCGGGA	CCTGGTGCCT	GCCACCAACT	ACAGCCTCAG	GGTGCCTGT	780
GCCAATGCCT	TGGGGCCCTC	TCCCTATGCT	GACTGGGTGC	CCTTTCAGAC	CAAGGGTCTA	840
GCCCCAGCCA	GCGCTCCCCA	AAACCTCCAT	GCCATCCGCA	CAGATTCAGG	CCTCATCTTG	900
GAGTGGGAAG	AAGTGATCCC	CGAGGCCCTT	TTGGAAGGCC	CCCTGGGACC	CTACAAACTG	960
TCCTGGGTTC	AAGACAATGG	AACCCAGGAT	GAGCTGACAG	TGGAGGGGAC	CAGGGCCAAT	1020
TTGACAGGCT	GGGATCCCCA	AAAGGACCTG	ATCGTACGTG	TGTGCGTCTC	CAATGCAGTT	1080
GGCTGTGGAC	CCTGGAGTCA	GCCACTGGTG	GTCTCTTCTC	ATGACCGTGC	AGGCCAGCAG	1140
GGCCCTCCTC	ACAGCCGC					1158

(14) INFORMATION FOR SEQUENCE ID NO. 13:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (2) MOLECULE TYPE: cDNA
- (3) SEQUENCE DESCRIPTION: SEQ ID NO. 13:

TGGATGGCAG TAAGGGAGG

(15) INFORMATION FOR SEQUENCE ID NO. 14:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (2) MOLECULE TYPE: cDNA
- (3) SEQUENCE DESCRIPTION: SEQ ID NO. 14:

CTTAAGAGGG GCAAACCTGG

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(16) INFORMATION FOR SEQUENCE ID NO. 15:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (2) MOLECULE TYPE: cDNA
- (3) SEQUENCE DESCRIPTION: SEQ ID NO. 15:

GCTTAGAGGA GGTGAGCCAG A

21

(17) INFORMATION FOR SEQUENCE ID NO. 16:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (2) MOLECULE TYPE: cDNA
- (3) SEQUENCE DESCRIPTION: SEQ ID NO. 16:

TGGGCAGTGC TGAGTTCC

18